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Wassilar cell adhesion molecule I signal sequence"
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US-09-832-658-7 x AAY70866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID AAY84950 standard; Protein; 166 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq_name: [Stief] is add a is associate to soil out in Abbody DAL (AAK84 vio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 124.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The patent discloses fusion proteins comprising alycosylated interferon-bota (IEN-bota) especially IFN Lota Ia, linker groups and non-IFN bota proteins, especially an immunoglobulin (1g) protein. The fusion protein is useful for inhibiting angiogenesis in a patient. In may also be used to treat multiple sclerosis, librasis, inflammatory and antoinmune discases, cancers, hepatitis and which intertion characterised by neovascularisation. The present sequence is a fusion protein that comprises histidine tag, an enteroximase linker and human IFN-bota-Ia. The His daged IFN-bota fusion construct was used as a template for mutagenesis in the construction of various mutant His tagged-IFN-bota expression plasmids.
15-00T-1999;
                                                                                                                                    Misc-difference
                                                                                                                                                                       Misc difference 8
                                                                                                                                                                                                            Mise-difference 5
                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                         cancer; autoimmune condition; tibrosis; lupus; multiple selerosis
viral disease; anglegonic disease.
                                    27 Mrs 2000.
                                                                         WO200023114 A2
                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       synthet.ic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alamine mutant of human interferon beta la protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 gScrScrAsnPheClnCysClnLysLeuTrp 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 TECTAGCAATTITCAGTGTCAGAAGCTCCTGTGG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 GlyAspAspAspAspLysMetSerTyrAssLeubesGlyPheLeuGlnAr L8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GGAGACGATGATGACAAGATGGCTPACGCCGCTCTTGGGAGCCCTACAAGC 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
99W0-US24201.
                                                                                                                                                                                                                              /note
                                                                                                                                                                                                                                                                   /note-
                                                                                                                                                                                                                                                                                                         Location/Qualitiers
                                                                                                                                                                                         /note
                                                                                                                /note-
                                                                                                                                                    /note
                                                                                                                                                                                         "wild type Leu replaced with Ala"
                                                                                                                                                                                                                                                                   "wild type Ser replaced with Ala"
                                                                                                              "wild type Ard replaced with Ala"
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10 AAY70872 standard: Protein: 166 AA.
                                                                                                                                                                                                                                                                    Seq_mame: [200753] Arathrichtenreit Archischt Gest AA2690 PATCAAY70872
                                            X E X E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.iun sed 1/1 to: AAY84950 from: 1 to: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New digrosylated interferon-beta-la coupled to a non-naturally occurring polymer containing a polyalkylene glycol useful for treating e.g. tumors, autoimmune disorders, viral infections and angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pepinsky B. Runkel L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                he used in the treatment of viral diseases, as well as in the treatment of and openic diseases. IFN-betala is useful as an agent for the treatment, remission or attenuation of a disease state, physiological condition, symptoms or etiological factors, or for their evaluation or diagnosis. The IFN-betala polymer conjugates may also be used for prophylaxis or treatment of any condition or disease state for which the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stay in the vasculature for longer periods of time, has increased stability in solution, reduced immunogenicity, protection of the modified IPN-beta-la from profeolytic diaestion and subsequent abouttion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY84950-64 represent alanine mutants of human interferon beta la (IFN-betala) protein. The protein is used to produce a composition comprising a diycosylated [FN-beta coupled to a non-naturally-occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI: 2000-339534/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity, and increased thermal stability. The polymer-based conjugates are useful for treating tumors and cancer, as well as autoimmune conditions such as tibrosis, lupus and multiple sclerosis. These may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymer containing a polyalkylene glycol. The composition has enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example to Page -: 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity, measured by an antiviral assay, as compared to physiologically active IFN beta. The polymer-IFN-betala conjugate has the ability to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFN-betala constituent is efficacious, in biological systems or specimens, note: the present symptome does not appear in the specification: it was created using information provided.
                                                                  Human interferon-beta alanine substituted mutant Al
angiogenesis; antisclerotic; antiinflammatory; immunosuppressive;
                                                                                                                   al-Jul-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 ATGGCTTACGCCGCTCTTGGAGCCCTACAAGCTTCTAGCAATTTTCAGTG 70
                                                                                                                                                                                                                                                                                                                       17 sginlysleuleufrp 22
                                                                                                                                                                                                                                                                                                                                                                 71 PRAGAAGETECTGTGG 86
                                                                                                                                                                                                                                                                                                                                                                                                             {\tt I-MetAlaTyrAlaAlaLeuGlyAlaLeuGlnAlaSerSerAsnPheGlnCy}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 114.00
                        interferon-beta: IFN-beta: immunoqlobulin; fusion profein; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9808-0104572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note- "Wild type the is substituted by Ala" Misc-difference 11
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              a human interferon beta alanine substituted mutant A: A. Taird by a human interferon beta alanine substituted mutant A: A. Taird by mutanting residues in the helix A of wild type sequence mutating residues in the Ala/Ser substituted mutants of IFN. beta having substitutions in the files A, B, C, D or E, or loops AB, C) or DE were assessed for helices A, B, C, D or E, or loops AB, C) or DE were assessed for helices binding and functional activities c.q. antiviral and antiprolliterative activities. The Al mutant shows antiviral and respect to receptor binding, compared to wild-type IFN. beta-la. The mutant can be used to produce IFN. beta fusion proteins.

Mote: The present sequence is not shown in the specification but is derived town with two beta-lations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WC200023472-A2.
                                                                                                                                                                                                                                        The patent discloses fusion proteins comprising alycosylated interferon-bota (IFN-beta) especially iFN-beta-la, linker groups and non-IFN-beta proteins, especially an immunoalcoulin (ia) protein. The non-IFN-beta protein is useful for inhibiting analogacies in a patient fusion protein is useful for inhibiting analogacies in a patient it may also be used to treat muttiple sclerosis, librosis, inflammatory and autoimmune diseases, cancers, hepatitis and viral intection and autoimmune diseases, cancers, hepatitis and viral intection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page ; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion proteins comprising interferon-beta-la useful for inhibiting
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derived from wild type human IFN-heta sequence found in page
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                and at least one removed amino acid residue comprisina an attachment aroup for the first non-polypeptide group. The invention also concerns reducing the immunogenicity and/or increasing functional in vivo half-life and/or serum half life of an interferon beta polypeptide comprising introducing an amino acid residue constituting an attachment group for a first non-polypeptide group into a position exposed at the context of 
                                                                                                                                                                                                                                                                                    Conjugates of the invention exhibiting interferon be a activity comprise at least one first non-polypeptide group covalently attached to an interferon beta polypeptide, the amino acid sequence of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim I); Page - ; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                multiple sclerosis comprises a non-polypeptide group covalently attached to an interteron beta polypeptide.
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07-FEB-2000; 2000DK-0000194
07-MAR-2000; 2000DK-0000363
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                                                                                                                                                                                                                                                            differs from wild-type human interferon beta in at least one introduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A conjugate exhibiting interferon beta activity useful for freating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pedersen AH. Schambye HT, Andersen KV, Bornaes C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W0200115736-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; interferon beta; antibody; multiple selerosis; deno therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human interferen beta saturt NIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents Human interferon beta mutant N4K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MAXY-) MAXYGEN APS.
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2000DK-0000642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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sarface of the protein that does not contain such a group and removing

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983938983333
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Percent Similarity: 81.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an amino acid residue constituting an attachment group for a first non-polypeptide group and subjecting the modified peptide to conjugation with the non-polypeptide group. The conjugate and a cell culture expressing the mutated polypeptides are useful in the treatment of discuse, especially multiple sclerosis, and for treating mammals having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutated proteins may be used for gene therapy. The DNA and proteins can also be used to treat viral infections (e.g viral hepatitis), cancer (e.g. breast cancer), inflammation, crohn's disease, acute myeloid leukhowia. Hodakin's disease and ulcerative colitis and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           circulating antibodies against interferon beta la or lb. DNA encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  derived from the human interferon beta sequence given in AAUOUU38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunomodulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human: interferon beta; antibody; multiple sclerosis; gene therapy; viral intection; viral hepatitis; cancer; breast cancer; inflammati crohu's disease; acute mycloid lcukucmia; Hodgkin's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human interfered beta metar* NAK/SETK/OROK/240K/885K/A89K
                                                                                                                                                                                                                                                                                                   /note- "Wild type Asm replaced with Lys" wise-difference 27\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-2001 (first entry)
                                                                                                                                                                         /note- "wild-type Glm replaced with Lys"
Misc-difference 85
                                                                                                                                                                                                                                                                  Misc-difference 39
                                                                                                                                                                                                                                                                                                                                        \begin{array}{ll} & \text{Location/Qualifiers} \\ \text{Misc-difference} & 4 \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                               Home suprens
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ulcerative colitis; immunomodulation; mutant; mutein; N4E, 507F 1 COF 140- 1875 M80F
                                                                                                                                           Misc-ditterence 89
                                                                                W0200115736-A2
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25-AUG-2000; 2000WO-DK00471.
                                         08-MAR-2001.
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 AA;
                                                                                                                                                                                                                                                                                    Znote: "Wild-type Arg replaced with Lys"
                                                                                                                                                                                                                                            /note- "Wild-type Asp replaced with Lys"
                                                                                                                       /note- "Wild-type Ala replaced with Lys"
                                                                                                                                                              /note= "Wild-type Glu replaced with Lys"
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Doroent Libertity: 77,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammation;
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alignment_scores
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                    seq_documentation_block:
                                                              scq_name: /2:DS1/qcgdata/geneses/deneseqp_cmb./AA2001.DAT:AAU00177
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21-OCT-1999; 99DS-0160782.
26-NOV-1999; 99DK-0001691.
07-FEH-2000; 2000DK-000194.
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14-AFR-2000; 2000PK-0000642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     circulating antibodies against interferon beta la or lb. DNA encoding the mutated proteins may be used for gene therapy. The DNA and proteins can also be used to treat viral infections (e.g. viral hepathis), concer (e.g. breast cancer), intlammation, Crohn's disease, acute myeloid leukaemia, Hodgkin's disease and ulcerative colitis and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and at least one removed amino acid residue comprising an attachment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              derived from the human interferon beta sequence i.len in A^{\rm AHO}00\,{\rm fB}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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AAU00177 standard; Protein; 166 AA
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                                                                                                                      17
                                                                                                                                                                71 TCAGAAGCTCCTGTGG 86
                                                                                                                                                                                                           1 MetSerTyrLysLeuLeuGlyPheLeuGlnArgSerSerAsnPheGlnCy 17
                                                                                                                 sGinLysLouLeuTrp 22
                                                                                                                                          The present sequence is not shown in the specification but is
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Ratio:
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                                   compension introduction is amino acid residue constituting an attachment in all for a first was polypepide droup into a position exposed at the cantaeve of the protein that does not contain such a droup and removing is amino acid residue constituting an attachment group for a first rad polypepide group and subjecting the modified poptide to conjugation with the rad polypepide it sp. the conjugate and a cell culture expression for instance of polypepides are useful in the treatment of
                                                                                                                                                                                                                                                                                                                                                                              troup for the first non-polypeptide group. The invention also concerns reducing the immanablementry and/or increasing tunotional in vivo half life and/or second half life of an interferon beta polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NMECH (William ACC) 1871 (1.14) 1874. Where we conjugate at least one cashibition interference between the acceptance at least one interference of which interference between 1972 bullians interference between 1972 bullians interference between 1972 bullians interference between 1972 and trached to an interference of which terrestrains wild type bullians interference between the track one introduced and a least observed unitary actification of the first an attachment and the state of the configuration of the state of the configuration.
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vital interfion: vital bepatitis; encor; broast cancer; inflammation;
'colm's discuse; reste mycloid leukaemia; Hodakin's disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MΛ
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especially multiple selectosis, and for treating mammals having
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Wild type the replaced with Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atte odda Frim.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Wild type And replaced with 152"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Wild type Ash replaced with Lys"
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aliqnment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alian sea 1/1 to: AAU00177 from: l to: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                             Zhote
Misc-difference 89
                                                                                                                                                                                                                                    /hote
Mise-difference 85
                                                                                                                                                                                                                                                                                                                  /note-
Misc-difference 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               circulating antibodies against interteron beta is on the DNA escading the mutated proteins may be used for sene thorapy. The DNA and proteins can also be used to treat viral intections (e.g. viral hepatitis), concertions (e.g. breast cancer), inflammation, Crohn's disease, acute nyeloid
                                                                                                                                                                              /bote
Mise-difference 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         viral infection; viral hepatitis; cancer; breast cancer; int.ammatious
Cyphe's disease; woute myeloid leukaemia; Hodykin's disease;
21-OCT-1999;
                 27-AUG-1999;
                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       046, 5278, 21396, 1436, 1859, [A866] F11.5k.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ulcerative colitis; immunomodulation; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; interferon beta; antibody; multiple sclerosis; dene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human interferon beta matant N4E, F27E, 5-446, 5446, 3 8FE/APPF, 7 123R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 166 AA;
                                                   25-AUG-2000; 2000Wn-DK90471
                                                                                           08 MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU00184 standard; Protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 derived from the human interteron beta sequence given in AAUUUUU88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    looker that Helsphin's disease and diserative collities and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunomodulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 TCAGAAGCTCCTGTGG 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is not shown in the specification but is

    [1] Jacq Edin, Johnson G. Berner ed H. Lend J. MAZ of L. DALL MARROWS LOS

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 9908-0160782
                 99DK-0001197
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                           49
                                                                                                                                                                                                                                                                                                                                                               /note- "Wild-type Asm replaced with Lys"
27
                                                                                                                                                               /mote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.818
                                                                                                                                                                                                                                                                                                        /note
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                                                                                                                                                               "Wild type Lys replaced with Ard"
                                                                                                                                                                                                                                                                                                                                            "Wild-type Arg replaced with Lys"
                                                                                                                                                                                                "Wild type Ala replaced with Lys"
                                                                                                                                                                                                                                  "Wild type Glu replaced with Lys"
                                                                                                                                                                                                                                                                      "Wild-type Gla replaced with Lys"
                                                                                                                                                                                                                                                                                                        "Wild type Asp replaced with Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
Percent Identity:
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ΞX
                                                                                                                                                                      seq_name: /83181.4 (1d)* (, decrees) Transacif combl/AA2001.DAT-AAH00185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity: 81.818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seq 1/1 to: AAU00184 from: 1 to: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 · NOV · 1999; 99DK · 0001691
07 · FEB · 2000; 2000DK · 0000194
07 · MAR · 2000; 2000DK · 0000363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          least one removed amino acid residue comprising an attachment group for the first non-polypeptide group. The invention also concerns reducing the immunoscolicity and/or increasing functional in give half life and/or second half-life of an interferon bota polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multiple sclerosis comprises a non-polypeptide group covalently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MAXY-) MAXYGEN APS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an amino acid residue constituting an attachment group for a first non-polypeptide group and subjecting the modified peptide to conjugation with the non-polypeptide group. The conjugate and a cell culture expressing the mutated polypeptides are useful in the treatment of
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16-MAY-2001 (tirst entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note: "Wild-type Arg replaced with Lys" Misc difference 39 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note- "Wild-type Asn replaced with Lys" Misc-difference 27\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "Wild-type Glm replaced with Lys" Mise\mbox{-}difference 85
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26 NOV-1999;
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                                                                                                                                               exhibiting interferon beta activity comprise at least one first non-polypeptide group covalently attached to an interferon beta polypeptide, the amino acid sequence of which differs from wild-type human interferon beta in at least one introduced and at least one removed amino acid residue comprising an attachment least one removed amino acid residue comprising the inwantion also concerns group for the first non-polypeptide group. The invention also concerns group to the immonogenicity and/or increasing functional in vivo half-life and/or serum half-life of an interferon beta polypeptide half-life and/or serum half-life of an interferon beta polypeptide tomprising introducing an amino acid residue constitution an attachment group for a tirst non-polypeptide group into a position exposed at the group for a tirst non-polypeptide group into a position exposed at the group for a tirst non-polypeptide group into a position oxposed at the
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an amino acid residue constituting an attachment group for a first non-polypeptide group and subjecting the modified peptide to conjugation with the non-polypeptide group. The conjugate and a real culture expressing the mutated polypeptides are useful in the treatment of disease, especially multiple sclerosis, and for treating mammals having circulating antibodies against interferon beta la or 1b. DNA encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page - ; 108pp; English.
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                 be then than that between human fibroblast IFN and human lymphoblast IFN. Kadhouctively labelled offices IFIA and IFIB (AAN19944, AAN19945) were used as initiators for the preprior buman fibroblast IFN.
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also be used to treat vital intections (e.g. Vital Impatifis), cancer
(e.g. breast ember). Intlammation, Crobu's disease, sent empedoid
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                                                                                            meanse IEN initators IEIA and IEIB and human libroblast IEN is
                                                                                                             It is predicted that the probability of complementarity between
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  the transcript derived using IFIA is given in AAN10046.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        x888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seq 1/1 to: AAP10052 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US:09 832-658-7 x AAP10052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19:JAN-1982;
03:FEB-1983;
15-JUL-1985;
The inventors claim a multiclass hybrid interferon polypoptide and a IMAA unit having a nucleotide sequence which encodes it. Fret the AA sequence consists of alpha and beta interferons. Fret. IFL is (i) the 1-73 AA seq. of HuIFN alpha 1 (and IF2 is the 74 M% AA seq. of HuIFN-alpha-61a (see AAN30155, AAN30222); or (ii) the 1-41 AA seq. of HuIFN-alpha-61a (and IF2 is the 44-16% AA seq. of HuIFN beta 1) (see AAN30150, AAN30222).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the 5' terminal of human fibroblast IFN. The entire sequence of mature human fibroblast interferon is encoded by AAN10049 (see also MADP10051). Another recombinant IFN which was recovered differed the AAN10049 in that the coden for the 50th unino acid had a "silent" base change (TAC to TAT), indicating the existence of genic polymorphism (see AAP10052/N10051).
                                                                                                                                                                                                                                                                                                                                                                                        Multi:class hybrid interferon poly:peptide(s) - with restricted antiviral and cell growth regulatory activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAN30152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W08302461-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hybrid interferon; antiviral; therapy; cancer; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pDM101/1rp/beta-1.
                                                                                                                                                                                                                                                                                                               Example: Fig 5; 6lpp: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1983-723186/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mark DF, Creasey AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 JUL-1983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of interteron (HulfN) -beta-1 encoded by plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP30219 standard; Protein; 165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 ATGGCTTACGCCGCTCTTGGAGCCCTACAAGCTTCTAGCAALLTTCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 sCluLysteuLeuTrp 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 FCAGAAGCTCCTGTGG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetSerTyrAsnLouLouGlyPheLouGlnArqSerSerAsnPheGlnCy 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85US-0755265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83US-0463574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8208-0440782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.818
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Σ Σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seal Laster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity: 81.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \frac{1}{4}n seq 1/1 to: AAP30219 trom: 1 to: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-IF and IF2 is the carboxy terminal of an alpha-IF (esp. the 17% seq. of HuIFN-supha-1 and the 74-167 seq. of HuIFN-supha-1 resp.) (see AAN30155, AAN30152). In the examples plasmeds pow5 and phM101/2:p/Weta-1 and platpha-41A were used (see AAN30151, AAN30152). HintI was used to diagest the DNA sequences in the region of sugnitional handleaps (see AAN30153, AAN30154, AAN30159), and the restriction tragments were ligated to form hybrid DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       )9-832-658-7 x AAP30219
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                                                                                                                                                                                                                                                                                                                                                                                  New modified human beta interferon polypeptide(s) - prepd. by plasmid transformed bacteria, with improved antiviral, anti-proliterative and immune regulating actions
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breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts
                                                                            Compared with interferon beta propd. by recombinant methods, the INES of the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial
                                                                                                                                                                                                                                                                                                Claim 16; Chart 2c, page 34; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAN50025
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84GB-0012564.
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/409data/4enese4/4enese4/p cmbl/AA1985.DAT:AAP50026
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Ratio: 4.944
Percent Similarity: 81.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AAP50024 from: 1 to: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-832-658-7 \times AAP50024
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                                                    Compared with interferon beta prepd. by recombinant methods, the INFS of the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis, and better in the solubility and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiproliferative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP163993-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antiviral; cell growth regulator; immune system regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFNX 444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of new modified human beta interteron polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-SEP-1991 (first entry)
                                                                                                                                                                                Claim 18; Chart 2e, page 36; 71pp; English.
                                                                                                                                                                                                                         anti-proliferative and immune regulating actions
                                                                                                                                                                                                                                          New modified human beta interferon polypeptide(s) - prepd. by plasmid transformed bacteria, with improved antiviral.
                                                                                                                                                                                                                                                                                                       N-PSDB; AAN50027
                                                                                                                                                                                                                                                                                                                             WPI; 1985-311944/50.
                                                                                                                                                                                                                                                                                                                                                                    Bell LD, Boseley PG,
                                                                                                                                                                                                                                                                                                                                                                                                         (SEAR ) SEAFLE G D & CO.
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Sequence
                                       stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 TCAGAAGCTCCTGTGG 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 AA;
166 AA;
                                       They are also easier to recover from incubation mixts
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About: Results were produced by the GenCore software, version 4.5 \times 10^{-10} copyright (e) 1993-2000 Computen LLd.
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Wnt-2 protein - mouse
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   probable cytochrome C-type blog
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pir2:T18314
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A:Molecule type: mRNA
A:Molecule type: mRNA
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A:Residues: 1-187 <TAN>
A:Cross-reterences: GR:Vou546; Nib:u32735, PIGM.CAA23837.1; PID:u327346
A:Cross-reterences: GR:Vou546; Nib:u32735, PIGM.CAA23837.1; PID:u327346
R.Derjick, R.; Centent, I; Derlered, E; Volckaert, G.; lavernict, J.; laveus, R.; Fi
R.Derjick, R.; Centent, I; Derlered, E; Volckaert, G.; lavernict, J.; laveus, R.; Fi
R.Derjick, R.; Centent, I; Derlered, E; Volckaert, G.; lavernict, J.; laveus, R.; Fi
Rature 285, 542-547, 1980
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Gene 10, 11-15, 1980
A:Title: The nucleotide sequence of human fibroblast interferon cDNA
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C:Species, Homo sapiens (man)
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Proc. Natl. Acad. Sci. U.S.A. 78, 5305-5304,
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A; Residues: 1-187 <LAW>
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R;Houghton, M., Baton, M.A.W.; Stewart, A.G.; Smith, J.C.; Doel, S.M.; Cartlin, G.H.;
Nacleic Acids Res. 8, 2885-2844, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A91468; MUID: 81005095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: The complete amino acid sequence of homan fibroblust interferon as deduced a A;Reference number: A93706; M0ID:81053720 A;Accession: A93706
                                                                                                                                                                                                                                                                                 A.Titje: Assignment of the disulphide bonds of lookeryte interferon A:Peference number: A93244; MUID:81123883
A.Contents: amporation; disulfide bond
E.A. Contents: amporation; disulfide bonds of lookeryte interferon
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A; Rosidues: 1.68 < HO2>
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A; Residues: 1 187 < HOU>
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A; Residues: 1 187 CDEPS
         A:Molecule type: mRNA
A;Residues: 71-161, Y;163-187 <SHE>
A;Residues: 71-161, Y;163-187 <SHE>
A;Experimental source: variant, clone pE526
A;Note. the loss of Cys-162 (and of the ability to form the essential disultide bond)
                                                                                                                                                                                                                                                                                                                                                                                 Nature 289,
                                                                                                                                                                                                                                                                                                                                                                                                                         R; Wetzel,
                                                                                                                                                                                                 Nature 294, 563-565, 1981
Affilie: A single amino acid change in IEN beta 1 abolishes its inticital activity.
                                                                                                                           A: Acression: A93269
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E hypothetical protein 17610.
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Activises in the relationship between human interferon alpha-1 and hera-1 genes. Aspecterone numbers (55.015; MRHJ:8603565)
AsA sessions (55.015)
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Bur. J. Brochem. 181, 645–653, 1989
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C;Genetics:
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RibelVeechio, V.G.: Kapatral, V.: Pedkar, R.J.: Patra, G.: Majer, C.: Les, I.: Le ever, M.: Meyer, M.: Ceitsman, E.: Selker, E.: Elzer, P.B.: Hethus, S.: o'Calladhan, D.: Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A.Wille: Who geneme segrence of the facultative intrarellular patragen Brusella medit A:Reference number: AD3252; PMID:11756688

A:Accession: AH4568
                                                                                                                                             submitted to the EMRC Data Library, November 1996
A;Reference number: Z19257
A;Accession: T28927
A;Status: preliminary: translated from dB/FMRP/DDR/
                                                                                                                                                                                                                                                                                                                                                                                                          C)Species: Caemorhabditis elegans
C)Date: IS out 1999 #sequence_revision IS out 1999 #fext change 15 out 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acrifiavin resistance protein F [imported] - Brucella melitensis (strain 16M)
C.Species. Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #t-xt_change 15 Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Map position: (1
C:Superfamily: hypothetical protein 62075
A; Experimental source: clone D1086
                                      A:Cross-reterences: EMBL:281491; PIDN:PAB64623.1; GEPBEGN00023; CESE:01685.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein D1086.6 Caenorhabditis elegans
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US-09-832-658-7 x Tll189
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Ratio: 2.405
Percent Similarity: 65.625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 ProAspThrMetAlaSerSerValAlaThrProLeulleLysGlnPheGl 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 ThrileSerLeuGlnTrpLeuThrProThrLeuTyrProTyrLysAsnle 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCGGAGACGATGATGACAAGATGGCTTACGGCGGTCTTGGGAGCGCTACAA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 ACGATGACAAGATGGCTTACGCCGCTCTTGGAGCCCTACAAGCTTC1 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .: Kapatral, V.: Bodkar, R.J.: Patra, G.: Mojor, C.: Log. L.: By
Esman, E.: Solkov, E.: Elzer, P.H.: Hedius, S.: O'Calladhan, D.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 87.500
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A: Map position: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riloda, M.; Shirdo, I.; Minoshima, S.; Shimizu, N., Toya, S.; Uyomura, K. Hiothem. Biophys. Res. Commun. 196, 468-472, 1993
A;Fille: Molecular clouling of cDMA encoding human drebrin E and chromosomal mapping of A;Beterence number: JN0809; MUID:9404036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aliqument_block:
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A:Residues: 1 649 <TODS
A:Cross-reterences: DDHJ:D17530; NID:q498650; PIDN:HAA04480 1: PID:q498651
A:Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Date: 14-Jul 1994 #sequence_revision 14-Jul-1994 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drebrin E (clone qDbhl3) - human
C:Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: pir2:JN0809
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Percent Similarity: 70.833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 5
C;Keywords: actin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Comment: This protein is an actin-binding protein.
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                                           hypothetical profess (man) ClSpecies: Homo sapiens (man) ClSpecies: Homo sapiens (man) ClSpecies: 20.869-1999 #sequence_revision 20-869-1999 #text_change 20-869-1999 ClArcession: I1476 ClArcession: I1476 R.W.I. Gassenhuber, J.: Wiemann, S. R.W.Imhnitt, R.: Heubner, D.: Mewes, H.W.: Gassenhuber, J.: Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the Protein Sequence Database, August 1999
A:Reference number: Z18181
                                                                                                                                                                                                          seq_name: pir2:f14763
                                                                                                                                                                  seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aliquiseq 1/1 to: JN0809 from: 1 to: 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 yAluAsuPhedinCysScrLys 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 FAGGAATTITCAGTGTCAGAAG 77
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                                                                                                                                                                                                                                                           53 uLeuSerGlyHisPheGluAsnClnLysValMetTyr 65
                                                                                                                                                                                                                                                                                                                                                 51 GOTTOTAGCAATTITCAGTGTCAGAAGCTCCTGTGG 86
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Percent Identity: 41.379
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A;Cross-references: EMBL:AL110225
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A;Ecsidues: 1:651 :WAM>
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A;Status: preliminary
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US-09-832-658-7 x T14763
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Percent Similarity: 79.310
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A; Residues: 1-707 <SHI>
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A;Accession: S60588
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Neuroreport 3, 109-112, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X59267; NID:9297820; PIDN:CAA41957.1; PID:9297821
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Ratio: 2.152
Percent Similarity: 79.310
probable pts phosphocarrier protein hpr - Chlamydia trachomatis (serotype D, strain H
CrSpecies: Chlamydia trachomatis
                                                                                   seq_name: pir2:D71528
                                                                                                                                                                                                                                                                                             Align seg 1/1 to: S60588 from: 1 to: 707
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                                                                                                                           53 ubeuserGlyHisPheGluAsnGlnLysValMetTyr 65
                                                                                                                                                                      51 .GCTTCTAGCAATTTTCAGTGTCAGAAGCTCCIGTGG 86
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Gaps: 1
Percent Identity: 41.379
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G:Date: 13-Sep-1998 #Sequence_revision 13-Sep-1998 #fext_chande 08-Oct 1999 G:Date: 07-Sep-1998 #sequence_revision 13-Sep-1998 #fext_chande 08-Oct 1999 G:Accession: D71528 #Sequence_revision 13-Sep-1998 #fext_chande 08-Oct 1999 Setting 08-Oct 1999 #sequence_revision 13-Sep-1998 #fext_chande 08-Oct 1999 #sequence_revision 13-Sep-1998 #sequence_revision 13-Sep-1998 #fext_chande 08-Oct 1999 #sequence_revision 13-Sep-1998 #fext_chande 08-Oct 1999 #sequence_revision 13-Sep-1998 #fext_chande 08-Oct 1999 #sequence_revision 13-Sep-1998 #sequence

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PrN-Hind, J.: Breton, G.: Smelchenko, M.V.: Markarova, K.S.: Zeng, Q.: Gibson, R.: Lee J. Bolly, M. L.: Bennadt, G.N.: Kennin, E.V.: Smith, F.R. Lee J.: Bacteriol. Bake 4 May 4 4 May, 2501 Comparative Analysis of the Solvent-Producing Hacterium Cle Acteries of number: Associated Comparative Analysis of the Solvent-Producing Hacterium Cle Acteries number: Associated MULLICAL FORZER EMBELLISTERS.
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                                   A:Experimental source: serotype b, strain UW 5/6x
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Acheterence number: A/15/0; MULD:99000809
Achetessian: 1/15/0
'pxb protein (336387) | imported; A
'.Species: Agrobacterion tumetaciens
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Percent Similarity: 85,714
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Primestal source: Clastridium acctobutylicum After824
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                                                                                Agrobacterium tumetaciens (strain 058, Cercon)
                                                                                9 GATGATGACAAGATGGCTTACGCCGCTCTTGGAGCCCTACAAGCTTCTAG 58
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R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; erado, G.; Cillet, W.; Grant, C.; Grentheer, C.; Kutyacin, L.; Lovy, R.; Li, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polysaccharide export protein bexD [imported] - Adrobacterium tumefaciens (Strain C58 C)Species: Adrobacterium tumefaciens ()Datc: 11-Jan 2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1 300 <KUI
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A.: Liu, F.: Wollam, G.: Allinger, M.: Donabty, D.: Scott, C.: Lappas, C.: Markelz,
Science 294, 2322-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Karp, P.; Romero, P.; Zhang, S. selence 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C: Accession: AE3088
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C:Accession: E98198
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                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain C58 (Dupont)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Authors: Yoo, H.; Fao, Y.; Biddle, P.; Jung, M.; Krespun, W.; Perry, M.; Serben Kall
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US-09-832_658-7_x_E98198
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Align seg 1/1 to: AE3088 from: 1 to: 300
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                                                           US-09-832-658 7 x AE3088
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C;Aceression: AD2066
K;Kanek III. Mikharta Y. Welk C.P. Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriquel
Nakaraki M. Shimpo, S.: Suqimoto, M.; Fakazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DRA Res. 8, 205-213, 2001
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A:Exp-originarial source strain PC1 7120
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A:Molecule type: PNA
A:Residues: 1-420 xKHR>
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C:Superfamily: cobalamin biosynthesis protein D
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Nakaraki, M.: Shimpo, S.: Sugimoto, M.: Takazawa, M.: Yamada, M.: Yasuda, M.; Tabata,
DNA ROS. B. 205-213, 2001
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                                                                                                                                                                                                                                                           A:Title: Complete Genomic Sequence of the Filamentons Nitrogen-fixing Cyanobacterium And A:Reference number: AB1807: MUID:21595285; PMID:11759840 A:Accession: AB2255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
polyphosphate kinase [imported] - Anabaena sp. (strain PCC 7120)
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                                                                                        A:cross-references: GB:BA0000019, PIDN:BA075292.1; PID:q17132726; GSPDR-GN00179
A:E-p-:[s-ctal secree: sisain pr. 7120
                                                                                                                                                           A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-736 KKUR>
A;Gene: alr<sup>4593</sup>
C;Superfamily: Escherichia coli polyphosphate kinase
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Percent Similarity: 65.385
                                                                   C;Genetics:
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Ference number: AB1807; MRID:21595285; PMID:11759840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 CAATITICAG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 ATGAMAGATGGCTTACGCCGCTC.....TTCCGACCCCTACAA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 thouAlaSerCysPheAlaboulgsSer 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 GCTICIAGCAATTTTCAGTGTCAGAAGC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 MetThrArqTrpLeuAsnProValLeuAlaIleAlaLeuGluSer1leMe 93
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aliqument_scores:

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R.Mindell, D.P.; Sorenson, M.D.; Dimcheff, D.E. proc. Natl. Acad. Sci. U.S.A. 95, 10693-10697, 1998 A; Title: Multiple independent origins of mitochondrial gene order in binds. A; Relevence number. 217242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: milocholidical Kirca amaticana (4) (2) #text_change 20-dun-2000 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-dun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: pirz:Tili68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Cross-references: EMBL:AF090339; NID:q4894475; PID:q4894477; PIDN:AAD:2504.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A: Molecule type: DNA
A: Residues: 1 346 < MIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: T11168; T11417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - greater thea mitochondrion C:Species: mitochondrion Rhoa americana (greater rhea, common thea)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_bioch:
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Percent Similarity: 85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Genome: mitochondrion
A;Genetic code: SGC1
A;Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA A; Residues: 1-44, 'T',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: Z17270
A;Accession: T11417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Keywords: membrane-associated complex; mitochondrion, MAD; exidative phosphorylatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL;Y16884; PIDN:CAA76502.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seq 1/1 to: AB2255 from: 1 to: 736
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R;Okutsu, T.; Kuroiwa, Y.; Kagitani, F.; kai, M.; Aisaka, K., Tsutsumi, C.; Karoko, Y. J. Biochem. 127, 475-483, 2000
A;Title: Expression and imprinting status of human PEGB/IGFZAS, a paternally expresse A;Reference number: JC7217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aliqnment_block:
                                                                                                               c,bate, op Junižõõõ #sequebee_rovialos 69 Jun 2000 #foxt_change 18 Aug 2000
C:Accession: JC7217
                                                                                                                                                                                                                                                                                   suq_name: pir2:JC7217
                                                                                                                                                                             C; Species: Homo sapiens (man)
                                                                                                                                                                                                         paternaily
                                                                                                                                                                                                                                     seg_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: T11168 from: 1 to: 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US = 09 - 83\overline{2} - 658 - 7 \times T11168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 ACCCCCCTTTTTCCAGCCCTACAACCTTCTAGCAATTTTCAGT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 ThrMetMetThrSerTrpThrLysThrProlleLeuAsnAlaThrLeuMe 245
                                                                                                                                                                                                                                                                                                                                                       245 tLeuAlaLeuLeuSerLeu 251
                                                                                                                                                                                                                                                                                                                                                                                                            54 TCTAGCAATTTTCAGTGTC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 AUGATUATUACAAGATGGCTT...ACGCCGCFCFFGGAGCCCTACAAGCT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . preliminary, translated from ca/EMRI/DDBJ
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Ratio:
                                                                                                                                                                                                      imprinted protein FEGB/IGF2AS [imported] - human
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SWISSPOOL 40:TREE_CHICK
SWISSPOOL 40:TREB_RIVU
SWISSPOOL 40:TREB_YEAST
SPOOL 40:TREB_YEAST
SPOOL 40:EYA4_FUGRU
SPOOL 40:EYA4_FUGRU
SPOOL 40:EYA4_FUGRU
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Swissprot 40 HRC2_MODSE
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-ModEL frame:_n2p.model -DEV-xlh
-0 /\quad_\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/\data=\/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Date: net 9, 2002 3:16 PM
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Database sequences: 105224
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SwissProt_40:PLSB_MOUSE -
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swissprot_40:PEGF_ECOLI .
swissprot_40:PEGF_ECOLI .
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Swissprot_40:PPM3 Monse .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SwissProt_40:XPOT_HUMAN +
SwissProt_40:MCRA_ECOLI -
SwissProt_40:FIXA_RHILP -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strd Orig
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Nucleic Acids Res. 9:1045-1052(1981).
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"The nucleotide sequence of human fibroblast interferon cDNA.";
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Houdhton M., Edton M.A.W., Stewart A.G., Smith J.C., Doel S.M.,
Cartiin G.H., Lewis H.M., Patei T.F., Emtage J.S., Carey N.H.,
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Nucleic Acids Res. 8:4057-4074(1980).
MEDLINE=81053854; FubMed-6159597;
Houghton M., Stewart A.G., P.∞) ≤ M., Emtado T.S., Eaton M.A.W
                                                                                                               Interferon Res. 5:521-526(1985)
                                                                                                                                                                       the relationship between human interferon alpha I and beta I
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    COLORA MW
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                                                                                                                                                                                                                                                                                                                                                                                         Autiviral;
                                    ZELIM AVE 004-119
                                                                        LUSS OF ANTIABAL WILLALLY).
                                                                                                                    TO FORM THE ESSENTIAL DISULFIDE BOND,
                                                                                                                                                                                                                            N LINKLIP CHAPTER.
                                                                                                                                                                                                                                                                         INTERFERON BELA.
            OBOT 3D4 O8 / 72 34 BC CRC 64:
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aliqument_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                 종주포존족족 중중
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: SwissProt_40:DREB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio: 4.944
Percent Similarity: 81.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seq 1/1 to: INB_HUMAN from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-832-658-7 x INB_HUMAN
                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and Lot commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pisher L.W., McBride O.W., Filpula D., Ibaraki K., Yound M.E.: "Human dichrin. (DWA sequence) mRWA tissue distribution and chromosomal localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo Sapiens (Human).
Enkaryota, Metaesa: Cherdata: Craniata, Vertebrata: Enteleostomi:
Mammalla: Entheria: Primates: Catarrhini: Hominidae: Home.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drebrin E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-007-2001 (Rel. 40, Last annitation update)
                                  EMBI, 000802; AAA16256.1; ...
EMBI, D17530; HAA04480.1; ...
EMBI, HC000288; AAH00283.1;
MIM; 126660; ...
                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mapping of its gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDITINE-94030036; PubMed-8216329; Shimilas N., Toya S., Oyemsta K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurosci. Res. Commun. 14:35-42(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID 9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INBN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q16643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DREB_HUMAN
                                                                                                                         or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                             ACM POSTUMENT
                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.:
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem, Biophys. Res. Commun. 196:468-472(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning of cDNA encoding human drebtin E and chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE osteoblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                 InterPro:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 TCAGAAGCTCCTGTGG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 ATCCCTTACCCCCCTCTTGGACCCCTACAACCTTCTAGCAALFITCAGTG 7c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 MetserTyrAsnLeuLeaclyPheLeuCluArqSerSerAsuPheGluCy
                                                                                                                                                                                                                                                                                                                    BELLICATION: DREBRINS MIGHT PLAY SOME ROLE IN CELL MIGRATION, EXTENSION OF NEURONAL PROCESSES AND PLASTICITY OF DENDRITES RESERVED FURTHER, BLINDS ACTIN.
                                                                                                                                                                                                                                                                       PLACENTA, SKELETAL MUSCLE, KIDNEY AND PANCREAS
                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY, BRAIN NEURONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sGlmLysLeuLeulrp 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pro: IPR002108; Cotilin_ADF PF00241; Cotilin_ADF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                          The street series
                                                                                                                                                                                                                                                                                      BRAIN MEURENS. ALSO FOUND IN THE HEARL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Persont Identity: 77.278
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aliqument_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: SwissProt_40:DREB_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio: 2.152
Percent Similarity: 79.310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3222E
Align seg 1/1 to: DREB_HUMAN from: 1 to: 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 04-632-658-7 X DREB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                            338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART, SMARTO2; ADF; 1. Neurone.
Actin binding: Brain: Neurone.
SEQUIENCE 649 AA: 71425 MN: A17308705P032098 GP064:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drebrin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-843-1997 (Rel. 35, Created)
01-843-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NeuroReport 3:104-112(1992).
-i- FUNCTION: DREBRINS MIGHT PLAY SOME BOLE IN CRIT. MICRATION.
-XTENSION OF NEURONAL PROCESSES AND PLASTICITY OF DENDRITES,
RESPECTIVELY. BINDS ACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shirao T., Obata N., ebata K.:
"Cloning of drebrin A and induction of neurite-like processes in
drebrin-transferted cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_Tax [D-10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Eutel>ostomi:
Mammalia: Entheria: Kodentia: Schurognathi: Muridae: Murinae: Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKEH_KAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDITAR 92305233; PubMed 1611026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN WISTAR: TISSUE-Brain, and Hippocampus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 uLeuSerGlyHisPheGluAsnGlnLysValMetTyr 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 GCTTCIAGCAATTTTCAGTGTCAGAAAGCTCCTGTGG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 GlyserAspAspLeuLysteuAlaAlaSerGlyGluGlyClyLeuGlnGl 53
                                                                                                                                                                              the European Bioinformatics institute. There are no rest
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modified and this statement is not removed. Usage by an
                                                                                                    EMBL: X59267; CAA41957.1;
                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.eh/announce/
or send un cmail to licensedish-sib.eh)
                                                                                                                                                                                                                                        this SWISS-PROI entry is copyright. It is produced through a collaboration between the SWISS-Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3. GUNCAPOA FOATGAGAAGA FROM TTACGGCGCTCTTTGGAGCCCTACAA... 50
  Actin-binding; Brain: Neurone; Alternative splicing sequence 707 AA, 77471 MW; R5279RP6EP7RROAA CRC
                                          SMART: SM00102; ADF: 1
                                                          Ptam: PF00241: Cofilin ADE; 1.
                                                                           InterPro: IPR002108; Cotilin ADF
                                                                                                                                                                                                                                                                                                                                                                                                                        SHRCELLULAR LOCATION: Cytoplasmic apprehens sesmin from ALTERNATIVE PRODUCTS. MULTIPLE FORMS OF DEERNING FROM NEURAL ALTERNATIVE SPLICING OF THE STRULL DEERNIN GENE PRINCIPLEMENT
                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: DREBRINS ARE CLASSIFIED INTO TWO FORMS OF THE EMBEYONED TYPE (E) AND SEL FORM OF THE ADDIT TYPE (A) FIME COURSE OF THEIR APPEARANCE ARE DIFFERENT FROM EACH OTHER THEIR STRUCTURES ARE CLOSELY RELATED.
                                                                                                                                                                                                                                                                                                                                                                                   LISSUE SCECIFICITY: BRAIN NEIPONS
                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          obata N., obata K.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 41.379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT:
        BS279BF6EP7BROAA CRC64
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aliqnment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     084341;
16 007:2001 (Rel. 40, Created)
16-007:2001 (Rel. 40, Last sequence update)
16-007:2001 (Rel. 40, Last annotation update)
16-007:2001 (Rel. 40, Last annotation update)
Phosphocarrier protein HPr (Histidine-containing protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia trachomatis.
Bacteria; Chlamydiales, Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIHP_CHLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Clinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=D/UW-3/CX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=813;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 GlySerAspAspLeuLysLcuAlaAlaSerGlyGluGlyClyLeudIndl 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "denome sequence of an obligate intracellular pathogen of humans: \operatorname{chiamydia\ trachomatis:"};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIJINE-99000809; PubMed-9784136;
                                                                                                                                                                                                                                                                                                                                                                              the European Ricinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Davis R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS TROT entry is egypright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Edoinformatics institute. There are no restrictions on its
                                                                                                                                                                                                                                                EMBL; AE001306; AAC67932.1; -.
                                                                                                                                                                                                                                                                                                           or send an email to licensewish sib.ch).
                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and remnities requires a license agreement (See http://www.isl.sh.sh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GGAGACGATGACAAGATGGCTTACGCCGCTCTTGGAGCCCTACAA... 50
                                                                  InterPro; (PRO01020; PTS_HPr_bis, InterPro; (PR002114; PTS_HPr_ser) Pfam; PF00381; PTS-HPr; 1.
                                                                                                                                                                      InterPro, 1FR000032; HPr_protein
                                                                                                                                                                                                       HSSP; P08877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENZYME I. PHOSPHO-HFK THEN TRANSFIRS II TO THE PEPMPASE (E II/II). HPR IS COMMON TO ALL PTS (BY SIMILARITY). EROZME REGULATION: PHOSPHORYLATION ON SER-67 INHILITS THE PHOSPHORYL TRANSFEP FROM ENZYME I TO HPK (BY SIMILARITY). SUBCELLULAR LOCATION: Cyleplasmic (By Similarity). SIMILARITY. BELONGS TO THE HPP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE PHOSPHOENOLPYKUVATE DEPERMENT OF THE PHOSPHOENOLPYKUVATE DEPERMENT FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYKUVATE DEPERMENT SUGAR PHOSPHOTKANNEERASE SYSTEM (PTS), A MAJOR CARROHYDRATE ACTIVE SUGAR PHOSPHOTKANNEERASE SYSTEM. THE PHOSPHOKYL GROUP FROM PHOSPHOENOLPYKUVATE - TRANSPERMED TO THE PHOSPHORYL CARRIER PROTEIN HER HYPERMENT OF THE PHOSPHORY OF THE PH
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2.152
79.310
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                                                                                                                                                                                                                                                                                                                                                                                  Program and the
                                                                                                                                                                                                                                                                                                                                                                                                                       commercial
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Phosphotransierase system; Sugar transport; Phosphorylation; Complete proteome.

PHOSPHORYLATION (BY ENZYME I) (BY

SIMILAPITY)

PROSITE; PS00589; PTS_HPR_SER;

PROSITE; PS00369; PTS_HPR_HIS; FALSE_NEG

MOD_RES

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For our Stantarity: Respect
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Kanti S., Jattusco', Mariani M., Dixon M., Demoai b., Metea
Winter R., Robertson M., Axton R., Brown A., van Heyningen V
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Archosauria: Aves; Neoquathae; Galliformes; Phasianidae; Phasianinae;
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MAY_color (Bel. Co. Last sequence update)
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Type absent behel of 4 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           t send an email to license fish sib.ch).
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n. Met. Genet. Bill 24(free).
PUNCTI N. MAY BE INVELVED IN BEVELERMENT SECTED EYE (BY
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    TH, 17V33 ×
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C 081527BB45GBCDFF CRC64:
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alignment_block:
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US-04-832-658-7/rov x WNT2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                PIR; H36470; B36470.
PIR; A4355B; A43558.
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-I- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY HE SIGNALING MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence, chromosomal localization and developmental expression of the mouse intil-related gene.": Development 107:643-650(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1991 (Rel. 18, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                         Developmental protein; Glycoprofein; Signal, SIGNAL 1 25 POTENTIAL.
                                                                                                                                                                                                                                        PROSTTE: PS00246; WNT1; 1.
                                                                                                                                                                                                                                                                            PRINTS;
                                                                                                                                                                                                                                                                                              Ptam; PF00110; wnt; 1
                                                                                                                                                                                                                                                                                                                            MGD; MGI:98954; Wnt2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Expression of multiple nevel Weel, intelepolated genes during retain and adult mouse development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDITINE 91122634; Pubmed 2279700;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID 10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Monse).
Enkaryota: Metazoa: Chordata: Craniata: Vertebrata: Enteleostemi:
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P21552:
                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE WAT FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gavin B.J., McMahon J.A., McMahon A.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1991 (Ref. 18, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                 FERICARDIUM HEART, AND VENTRAL LATERAL MESUFERM, IN ABILITS IN
LUNG, BRAIN, HEART AND PLACENTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SEECIFICITY: IN EMBRYOS IN THE DEVELOPING ALLANIOIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    extracellular matrix
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                                                                                    Quality:
                                                                                                                                                                                                                                                              SMCO.
                                                                                                                                                                                                                                                                            PRO1349; WNTPROTEIN.
                                                                 Ratio:
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295
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N-LINKED (GLONAC: ...) (P
') SEC26'SFD381'SEF1D CRC64;
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seq_name: SwissProt_40:PLSB_MoUSE
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alignment_block:
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01-NoV-1997 (Rel. 35, Last sequence update)
16-007-2001 (Rel. 45, Last annotation update)
16-007-2001 (Rel. 45, Last annotation update)
Glycerol 4 phosphate acyltransferase, mitochondrial precursor
(EC 2.3.1.15) (GPAI) (P90).
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Mammalia: Entheria: Rodentia: Schurognathi; Muridac, Marinae: Mos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDITURE 92084678; PubMed 1721057.
Shin D. H., Paulauskis J.F., Moustaid N., Sul H.S.;
"Transcriptional regulation of p90 with sequence homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPAM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haio), Chom. 266:28834-28839(1991).

1- CAMINITIC ACTIVITY: ACY, CAA SIL-Glycore! 3-phosphare - COA + 1-
1- CAMINITIC ACTIVITY: ACY, CAA SIL-Glycore! 3-phosphare
1- CAMINAY: FIRSI SIRP IN DE BAVO PHOSPHOLIPID BIOGENESIS. II MAY
1- CAMINAY: FIRSI SIRP IN DE BAVO PHOSPHOLIPID BIOGENESIS.
1- ALISO FUNCTION IN THE REGULATION OF MEMBRANE BIOGENESIS.
1- ALIGO FUNCTION IN TOWATTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli glycerol-3-phosphate acyltransferase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 AGAGCGGGGTAAGCCATCTTGTCAT 13
                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way madified and this statement is not removed, usage by and for commercial entities requires a license agreement (See http://www.isb-sib.cn/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROJ Partry is copyright It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phospholipid biosynthesis: Transferase: Acyltransferase:
                                                                                                                                                                                                                                                                                       Transmembrane: Mitochondrion;
                                                                                                                                                                                                                                                                                                                         Plant PF01553; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                           InterPro: IPRO02123; Acyltransterase.
                                                                                                                                                                                                                                                                                                                                                              MGD; MGT:109162; Gpam
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                                                                         Quality:
                                                            Ratio:
                                                                                                                                                   827 AA:
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494
574
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                                                                                                                                                                                                                                                          ; Transit peptide.
HITECHONDRION (POTENTIAL).
GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE
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; A64EDE697BD564B3 CRC64.
                                                                                                                                                                                        CYTOPLASMIC (FÖTENTIAL)
POPENTIAL.
                                                                                                                                                                                                                                          MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
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seq_name: SwissProt_40:PLSB_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycerol-3-phosphate acyltransferase, mitochondrial precursor (EC 2.3.1.15) (GPAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPAM OR KIAA1560
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Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 AGCAATTTTC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-2000) to the EMBL/GenEank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCB1_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.: "Prediction of the coding sequences of unidentified human genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 167-828 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acyl-sn-qyverol 3-phosphate,
acyl-sn-qyverol 3-phosphate,
i-partimay; FIRST STEP IN DE NAVO PHOSPHOLIPJE BLOGSMEHESIS. IT MAY
ALSO FUNCTION IN THE REGULATION OF MEMBRANE BLOGSMESIS.
-i- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 7:273-281(2000)

-i- CATALYTIC ACTIVITY. Acyl-COA + sn-qlycerol 3-phosphate
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DNA Res. 7:273-281(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20450683; PubMed-10997877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. They use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBI outstation the European Bioinformatics institute. There are no institutions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See nttp://www.isb alb.th/newember/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Outer membrane (By similarity).
-!- SIMILARITY: BELONGS TO THE GPAT / DAPAI FAMILY.
                                                                                                                                                                                                                                                                                                                                                             MIM; 602395;
                                                                                                                                                                                                                                                                   Phospholipid biosynthesis: Transferase: Acyltransferase:
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                      93836 MW;
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                                             MITOCHONDRIAL INTERMEMBRANE (POTENTIAL)
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MIPOCHONDRION (POTENTIAL).
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1. Real Chem. 275 (1668-6167)(2000).

1. CALALYID ATIVITY: Acyl CoA - six alycerol 3 phosphate - CoA + 1
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SERVIN SERVIE CAMERY: CIESTE LIVER:
MEDITNE SERVICE OF SCIENTS CONTROL A.V., Medinsky C., Haldar D.,
MEDITNE SERVICE OF SCIENT SERVICE TRANSPORTATIONS and a gylosolic domain
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Mammaalia; Eutheria; Kodentia; Sciurodnathi; Muridae; Murinae; Kattus,
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15 H0 feet (Ref. 6) Last sequence update)
15 H1 feet (Ref. 8) Last annotation update)
                                              Phospholiped biosynthesis: Transferase: Acyltransferase:
Transmouthrane: Mitochondrion: Transit peptide.
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EMBL: F03771: AAR69426.22 ART INTE
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PARHMAY: FIRST SIDE IN DE WAVE EBESPOLIFIO BU SYNHEBSIS. II MAY
ALISO FINETION IN THE EDITIATION OF MEMBRANE BUJCHNISTS.
SUBCTELLUAR COTALIN INTERPRETATION OF MEMBRANE BUJCHNISTS.
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seq_name: SwissProt_40:DkEb_CHICK
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                                                                                        drebrin gene.";
Brain Res. Mol. Brain Res. 19:10?-114(1993).
1: PUNCTION: DEDRIKING MIGHT PLAY SIME REAL IN CELL MIGRATION,
EXTENSION OF NEURONAL PROPERTIES AND PLASTICITY OF DENERLIES.
                                                                                                                                                                                                 Kojima N., Shirao T., Obata K.; "Molecular election of a developmentally regulated brain proteins chicken drebrin A and its expression by alternative splicing of
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O1 NAV-1990 (Rel. 16, Created)
O1-NAV-1997 (Rel. 45, Last seguence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequences of two entryonic dreblins, developmentally regulated brain proteins, and developmental change in their aRNAs.": Brain Res. 464:207-215(1988).
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Eukaryota: Metazoa: Chordaiu: Craniata: Vertebrata: Eufeleostomi:
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1: SUBCELLUIAR LOCATION: Cytoplasmic.
1: ALTERNATIVE PRODUCTS: MULTIPLE FORMS OF DREBKINS RESULL FROM
ALTERNATIVE SPLICING OF THE SINGLE DREBKIN GENE DUKING NEURAL
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-1: MISCELLANDOS: DREBRINS ARE CLASSIFFED INTO TWO FORMS OF THE CHARACTERIST THE TOTAL CONTROL OF THE CHARACTERIST OF THE CHARAC
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cent Similarity: 79.310 Percent Identity: 37.931
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EMBL; 865289; AAB28012.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro: IPR002108; Cofilin_ADF
                                                                                    01-MAK-2002 (Rel. 4), Created)
01-MAK-2002 (Rel. 4), Last sequence update)
01-MAK-2002 (Rel. 4), Last annotation update)
interleukin-l beta precursor (IL-1 beta).
   Trichosurus vulpecula (Brush-tailed possum).
Enkaryota: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          send an email to license isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (7) GlyserAspAspLeuLysLeuAlaAlaSerGlyGlyClyGlyLeuLeuGt 53
                                                                                                                                                                                                                                                                                                                                                                                          53 utenserGlyHisPheGluileGluLysValMetTyr 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 AGCTTOTAGCAATTTTO'AGTGTCAGAAGCTOCTGTGG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R COMMANDATGARGACAAGARGCCTTACGCCGCTCTTGGAGCC...CTACA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THEIR STRUCTURES ARE CLOSELY RELATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBRYOMIC TYPE (E1 AND E2) ARE OUR FORM OF THE APHIT TYPE (A) TIME COURSE OF THEIR APPEARANCE ARE DIFFERENT FROM FACH OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  $65,291; AAH28012.1; JOINED $65,292; AAH28012.1; JOINED $65,294; AAH28012.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $65281; AAB28012.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S65280: AAR28012.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S65289; AAB28012.1; JOINED S65290; AAB28012.1; JOINED
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Ratio:
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                                                                                                                                                                                                                                                  STANDARD.
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125 K
552 E
571545 MW:
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MISSING (IN ISOFORM E2).
E -> EE (IN REF. 1).
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                                                                                                                                                                                                                                                      TRT:
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                                                                                                                                                                                                                                                            269 AA
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aliqnment_scores:
                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                         seq_name: SwissProt_40:Y871_METJA
                                                                                                                                                                                                                                                                                                                                                                                               Quality: 47.00
Ratio: 2.765
Fercent Similarity: 60.714
                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: IL1B_TRIVU from: 1 to: 269
                                                                                                                                                                                                                                                                                                                                           0S-09-832-658-7 \times 11.1B\_TRIVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILNE 1922:1014, Filamed three-2003;
Wedlock D.N., Soh L.P., Parlame N.A., Huddle B.M.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
NCBI_TaxID-9337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vet. Immunol. Immunopathol. 67:359-372(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning and physiological effects of brushtail possum interleukin-lbeta.", % \left( \frac{1}{2}\right) =\left( \frac{1}{2}\right) ^{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. Then
use by non-profit institutions as long a
goalitied and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                piam; pF02394; iil_propep; 1.
rKINTS, rS09262; iillHBGF.
proDom; pD002536; interleukin_1: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF071539; AAD21871.1; HSSP; P01584; 1HfB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (see http://www.licb.sib.eb/horement or send an email to licensedisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART: SM00125; IL1; 1.
PROSITE: PS0025; INTERLEUKIN_1; 1.
Cytokine: Macrophage: Mitogen; Infl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 269 AA;
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                 Q58281;
15-JUL-1998 (Rel. 36, Created)
                                         Y871_METJA
                                                                                                                                   33 sGlyTy:PheGlnTyrProAspLenCysSerLys 44
                                                                                                                                                                                                                  17 AspAspAspAspArqGlnPheTyrGluAlaAspGlyProAsuGlnLysLy 33
                                                                                                                                                                        56 TAGCAATTITCAG.....TGTCAGAAG 77
                                                                                                                                                                                                                                                         6 GACGATGATGACAAGATGGCTTACGCCGCTCTTGGAGCCCTACAAGCTTC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, H-CELL MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY. MATURATION ARE INVOLVED IN THE THYMACOPY RESPONSE, HEING IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO SIMULATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: MONOMER.

POMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUBGESTS THAT THE DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUBGESTS THAT THE AMINO ENDS OF THESE PROTEINS SHEVE SOME AS YET UNDEFINED FUNCTION. THE MISCELLANGOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR SPECIFIC SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS PRECURSOR SPECIFIC SUGGESTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
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[PR0003502; Interleukin_1_Prop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113
                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31141 MW;
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 1
Percent Identity: 42.857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERLEUKIN-1 BETA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inflammatory response: Pyroden.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
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                                                                                                                                                                                            of anameditation, block:
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SHEAR THE CONTROL FRANCE GLUCK. Thou I., Floischmann R.D., Button G.E., White C.A., Fitzberald L.M., Claytan R.A., Gordyne J.D., Satton G.E., White C.A., Fitzberald L.M., Claytan R.A., Gordyne J.D., Satton G.E., White Isoacherty H.A., Fomb J.F., Adams M.D., Reich C.I., Satton G.E., Fitzberaty N.S., Weitstock K.G., Merrick J.M., Glodek A., Seedt J.L., Groodbaren N.S. M., Weldman J.F., Fuhnmann J.L., Nanyen D., Brott J.L., Groodbaren N.S. M., Weldman J.F., Fuhnmann J.L., Nanyen D., Hiterbork F.E., Kelley L.M., Poterson I.E., Sachwert N.S., Bunn M.C., Gorden K.M., Hurst M.A., Kelder K.B., Herodewky M., Willey H.A., Kelder K.M., Smith H.O., Weese C.R., Venter J.C., "Nample to de Lowe Separate of the methamogenic archaeodo Methamogenic Allocations of the Control of Control
14 (4.7));
1 Nov 1995 (Ref. 42. Steaded)
Nov 1995 (Ref. 42. Start sequence update)
Nov 1995 (Ref. 42. Start annotation update)
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Battor (1866
Pent Stanifity. 75.000
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16 PH JOH (Re), 48 Last.
Hypothetical profess MJOW/1
MJOH/1.
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                                                                                                                                                             TEVEL ARIES
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! SIMILARITY. 10 MINOROL MAISSO AND MAISSO.
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                                                                                                                                                             SHANDARD
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General Identity: 40.000
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US:09-832-658-7 x YFB3_YEAST
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                                                                                                                                        Q1315; 015429; 093007; 016551; 012758; 09002; 0900X7; 16-007-2001 (Rel. 40, Created) 16-007-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last adjusted) update) Serine-project kinase AIM (EC 2.7.1.37) (Ataxia telandiratasia serine-project kinase AIM (EC 2.7.1.37) (Ataxia telandiratasia
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Barrell B.G., Churcher C., Rajandroam M.A.;
Submitted (SEP 1994) to the DMRL/Orniork/ODBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasandma S. I., Sasandma M., Tsychiya Y., Sowia F., Yokoyan
Yamazaki M., Tashiro H., Eki T.,
"Analysis of the nucleotide segrence of chromosome VI from
Saccharomycos corevisiae.";
Nat. Genet. 10:261-268(1995).
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Bukaryota; Fangi; Ascomycota; Saccharomycotina; Saccharomycetes.
SEQUENCE FROM N.A.
                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Home.
                                                                                         Homo sapiens (Human)
                                                                                                                              mutated) (A-T, mutated).
                                                                                                                                                                                                                                          ATM_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                           194 AshAsptystenThrPheAlaGlutenTyrVallenThrlleAlaThrSe 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: D50617; BAA09225.1; -. FMB: 144597; BAA09004.1; -.
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                                 NCBI_TaxID 9606;
                                                                  Bukaryota, Motazoa,
                                                                                                                                                                                                                                                                                                                                   210 rHeLysCysSerLysIleLeu 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGD; S0001881; YFL013C.
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Hyrd P.J., McConville C.M., Ceoper P., Barkhill J., Stankovic T.,
McGuire G.M., Thick J.A., Taylor A.M.R.;
"Nuturious revealed by sequencing the Schalf of the gene for ataxia
relangies
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Shiloh Y., Tagle D.A.
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66105020: Pubmed 8521392:
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                                    Sadamandan S N , Chessa L., Collins F.S.,
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MEDITINE-97294602: PubMed-9150358;
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Hobson K., Gatei M., Zhang N., Watters D., Ederton M., Shiloh Y.,
Ehartanda S., Kufe D., tavin M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97141775; PubMed-8988033; Jung M., Kondratyev A., Lee S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watters D., Khanna K.K., Beamish H., Birrell G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KINASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Khanna K.K., Keating K.F., Kozlov S., Scott S., Gater M., Indoom K.,
Taya Y., Gabrielli B., Chan D., Lees-Willer S.P., Lavin M.F.,
"ATM associates with and phosphorylates p54: mapping the region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Interaction between ATM protein and c-Abi in response to DMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97311400 - PubMed-9168117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 387:520-523(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           damage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "ATM binds to beta adaptin in cytoplasmic masicles.";
Proc. Natl. Acad. Sci U.S.A. 95:10146-10151(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P53 BINDING, AND KINASE ACTIVITY.
MENYIMP-99067381: PubMod-9843217:
                                                                                                                                                                                                                                                                               HIOSPHORYLATION OF P53, AND MUTAGENESIS OF ASP-2870 AND ASN-2875.

MEDLINE-98404274; PubMed-9733515;
Canman C.E., Lim D.-S., Cimprich K.A., Taya Y., Famai K.,
Sakaguchi K., Appella E., Kastan M.B., Siliciano J.D.;
Sakaguchi K., Appella B., Kastan M.B., Siliciano J.D.;
Mactivation of tex AVM kinase by ionizing radiation and phosphorylation of p53.";
Science 281:1677-1679(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                          Banin S., Moyal L., Shieh S.-Y., Taya Y., Anderson C.W., Chessa L., Shoroklinsky N.I., Prives C., Relss Y., Shiroh Y., 219 Y., "Enhanced phosphorylation of p53 by ATM in response to DNA damage."; Science 281:1674-1677(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lim D.-S., Kirsch D.G., Canman G.E., Ahn J.-H., Ziv Y., Newman h.S., Darnell R.B., Shiloh Y., Kastan M.B.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDI.INE=98374320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interaction."
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                                                                                                                                                                                                          Smith G.C.M., Cary R.R., Lakin N.D., Hann B.C., Teo S. B., Chen D.J.,
                                                                                                                                                                                                                               MEDIINE-99432198; PubMed:10500142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION OF P53
                              Cortex D., Wang Y., Oin J., Elledge S.J.:
"Requirement of ATM-dependent phosphory)ation of break in the DNA
damage response to double-strand breaks.":
                                                                   PHOSPHORYLATION OF BRCA1.
MEDIJINE=20018333; PubMed 10550055;
Cortez D., Wang Y., Qin J., Ellede
                                                                                                                                                                           "purification and DNA binding properties of the ataxia telanglectusia
                                                                                                                                                        gene product ATM."
                                                                                                                                                                                                                                                DNIGNIE ANG
                   Science 286:1162-1166(1999).
                                                                                                                                            Proc. Natl. Acad.
                                                                                                                                                                                              jackson S.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cenet. 20:398-400(1998).
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                                                                                                                                              Sci. U.S.A. 96:11134-11139(1999)
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seen decommendation block:
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iodu rabilpes (Japanese puttertish) (Takituqu rubilpes).
1 okuryeti: Medafeti "Tooddia) Charidata; Vertebrada: Enteleostomu;
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A vanthomerphas Acanthopteryaii: Percomerphas Tetraodomtitormes:
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i.oc.itsen' nometod 4 (Frankent).
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     PROPRESENTATION OF NUBBER.
MEDIENE 2022/912: FORMAN 10765245;
LUM DO SO, KEM SO TO, XUESO, MERCE KOSO, Lin Jo, Potribi JUHLJO,
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"RACC) a saper complex of RECAL associated meeting involves
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Gater M., Young D., Perosaletti K.M., Pesai Mehtu A., Spring K.,
Kartar S., Larras M.F., Satti K.A., Penerangan P., Khanna K.K.;
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Livitableo J.M., Weiver D.L.;
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1 @93mc2 rattus norvegicus (rat).
              ( 0957z4 casuarius casuarius
( 094d52 oryza sativa (rice)
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Q3p2w0 homo sapiens (human). F
Q3p2w1 abiotrophia defectiva.
Q5g254 pyroccomus korikoshii.
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098er5 rhizobium toti (mesorhiz
09xjj8 dunaliella saiina, chlor
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į @9n317 caeborhabditis ciegans
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seq_documentation_block:
TD 077812 PKELIMI
AC 077812;
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sp_bacteriap:Q98KL0
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                                                                                                                                                                                                              seq_name: sp_human:Q15943
                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                              Align seq 1/1 to: 077812 from: 1 to: 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity: 81.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08^{-}09 \cdot 832 \cdot 658 - 7 \times 077812
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (THEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca Tascieularis (Ciak calina Sacaque) (?premolens memkev).
Sakuryota: Metazoa: Chordata: Craniata: Vertebrata: Enteleostomi:
Mammalia: Eutheria: Primates: Catarrhini: Cercopithecidae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMAET, SM00076; IFabd; 1.

EROSITE; FSU0052; INTEPPERFON_A_B_D; 1.
Activitat; Cytokine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matheux F., Le Grand R., Rousseau V., De Maeyer E., Dormont D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE~99156140; PubMed=10048395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cercopithecimae: Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Macaque lymphocytes transduced by a constitutively expressed interferon beta gene display an enhanced resistance to SIVmac2sl infection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PROJETS6; INTERFERONAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00143; interteron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 187 AA; 22266 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000471; Interferon_abd.
                                                                015943
015943
01 NOV-1996 (TrEMBLrel: 01, Created)
01-NOV-1996 (TrEMBLrel: 01, Last sequence update)
01-DEC-2001 (TrEMBLrel: 19, Last annotation update)
Homo sapiens (Human).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
                                           INTERFERON-BETA PRECURSOR.
                                                                                                                                                                                                                                                                                                                                         22 MetSerlyrAshteulandlyPhoLeuGluArdserSerSerPhodimCy (8
                                                                                                                                                                                                                                                                                                                                                                                     21 AUGGCTTACGCCGCTCTTGGAGCCCTACAAGCTTCTAGCAATTTTCAGTG
                                                                                                                                                                                                                                                                                                     71 TCAGAAGCTCCTGTGG 86
                                                                                                                                                                                                                                                           sGlmLysLouLeuTrp 43
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                                                                                                                                                         PRELIMINARY;
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Gaps: 0
Percent Identity: 72.727
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                                                                                                                                                           PRT;
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1053 | 098k10 rhizobium lott (messo
74 | 0951b8 sus serota (pig) inte
84 | 0951b8 sus serota (pig) inte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 period framewoods county loss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acris seq 1/1 to: 215943 from: 1 to: 187
                                                                                                                                                                    MEDIANE 92 4489 60; PubMed 1640116;
Alternation E. J. Call A. Limbordson M., Abbandson M., Alm G.;
"Molecular clouding of a rope encoding porcine interferon beta.";
Limborton Res. 12-15 Clou(1992).

1. SUMILABITY: MEDIANCE CLOUCHER MATHEMER WALSHA, BECA ARC CHILA
EMBC: M90702: AAA3005031:
EMBC: 841178: AAB22723.1:
ECSE: F01574: LAUL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bukanyata: Metabas Chardata: Craniata: Vertebrata: Entebeastomi;
Mummatin: Erbarta: Setartiadactyla: Shina: Shidac: Sas.
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01 NoV 1996 (ITEMBLEEL 01, Last sequence update)
01 JUN 2001 (ITEMBLEEL 17, Last annotation update)
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Philos. Brins. R. Soc. Lond., B. Kiol. Sci. 299:29-86(1982).
P. SIMILAPTIY. DELSAGE CELHE INTERFED A AURIN, 60TA AND DELTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE ROOFSTOR POLANCE 6183692;
Fiers W., Femant E., Devos R., Cherontre H., Contrebas R.B.,
Sheysen I., Detruve W.M., Stundbedd P., Daverdier J., Laya Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WITH THE STATE THINK
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InterProp TPR (047): Interteron_abd
Plans PF20143: interteron; 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arturason K., 1961 A., Lindersson M., Johansson M., Aim
Arturason K., 1961 A., Lindersson M., Johansson M., Aim
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                                                                                                                                                                                                                                                                                                                                                                                                         TO THE MENT OF STREET, STREET,
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                                                                                                                                   YTTIMV 4
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Photoscopy (Liter belon_abd; 1)
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seq_name: sp_ordanelle:Q9XL23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TREMBLEEL 12, Created)
01-NOV-1999 (TREMBLEEL 12, Last sequence update)
01-DEC-2001 (TREMBLEEL 19, Last annotation update)
NADH-URIQUIRONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3)
Smithornis sharpel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                     EMBL: AF090340; AAD32523.1;
InterPro: IPR001750; oxidored_q1.
InterPro: IPR000266; oxidored_q1_N.
Plam: PF00361; oxidored_q1:1.
                                                                                                                               Sorenson M.D., Dimehett B.B., Ast J.C., Yuri T., Mindell D.F.: "Complete mitochondrial DNA sequences for tive birds and a turtle-standing (SF) 1-88) to the SMA, Sedimondrial DNA sequences, and to disclose the SMA Sedimondrial databases."

-1- CATALYTIC ACTIVITY NADB + SBIQUINGH: MADC) + DRIGHTMAL.
                                                                                                                                                                                                                                                                      "Interordinal relationships of birds and other reptiles based on whole mitochondrial genomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9XI,23;
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#Ittalandrian, MAD: %idoreductase; Ubiquinone,
SEQUENCE     459 AA; 51128 MW; 169A6450277c7ED1 CRC64;
                                                                                                                                                                                                                                     Syst. Biol. 48:138-152(1999).
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDITINE 98393707; PubMed 9724766; Mindell D.P., Sorenson M.D., Dimcheff D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9X1,23
                                    Ptam; PF01059; oxidored_q5_N; 1.
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               Yuri T.:
                                                                                                                                                                                                                                                                                                                                Mindell D.P., Sorenson M.D., Dimcheft D.E., Hasegawa M., Ast J.C
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       "Multiple independent origins of mitochondrial gene order in birds.": Proc. Natl. Acad. Sci. U.S.A. 95:10693-10697(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCB1_TaxID-81930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smithornis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archosauria: Aves; Neognathae; Passeritormes; Enrylaimidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteliostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00076; [Fabd;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probom; PD000550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 sGlmlysLouleu 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 FCAGAAGCTCCTG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 MetSerTyrAspValLeuArqTyrGlnGlnArqSerSerAsnheuAlaCy
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71.429
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aliqnment_scores:

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Seldocumentation_block:
10 065341 PRELIMIK
AC 065341 TERMELE
DI 01-AUG-1998 (TERMELE
DI 01-DEG-2001 (TERMELE
DE 801JUBLE ACID INVEKTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio: 4.417
Percent Similarity: 70.588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align set 1/1 to: 09XL23 from: 1 fo: 459
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πg-υ9 832-658-7 x o17729
                                                                                                                                            sel_name: sp_plant:065341
                                                                                                                                                                                                                                                                                                                                                                                                                          omality: 50.00 Length: 24
Ratio: 2.941 Caps: 0
Percent Similarity: 70.833 Percent (dentity: 45.83)
                                                                                                                                                                                                                                                                                                                                   Align seq 1/1 to: 017729 from: 1 to: 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metadoa: Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0) JAN 1598 (TEMBLEEL 05, Created)
01-001-2001 (TEMBLEEL 18, Last sequence update)
11-065 2001 (TEMBLEEL 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mment_scores:
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EMBL: 281491; CAB04023.2;
SEQUENCE 477 AA; 53218 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITINE 99069613; PubMod-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_[ax10 6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhabditidae: Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE EROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1996) to the EMBL/demBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 H 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 A 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 ThrileSerLeuGlnIrpLeuIhrProThrLeuTyrProTyrLysAssLe 52
065341;
01 ANG-1998 (TrEMBLrel. 07, Created)
01-ANG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
solUBLE ACID INVERIASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            investigating biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOHO!
                                                                                                                                                                                                                                                         103 AspaspVallysArgsluCysAlaAlaAla6lyslyAspTyrTyrAlacl 119
                                                                                                                                                                                    119 yAlaAsuPheGludysScrLys 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 ACGATGATGAGAAGATGGCTTACGCCGCTCTTGGAGCCCTACAAGCTTCT 56
                                                                                                                                                                                                                         56 FAGCAATTTTCAGTGTCAGAAA 77
                                                                                                                                                                                                                                                                                               6 GAUSATGATGAGAASATGGCTTACGCCCCCTTTGGAGCCCTACAAGCTTC 55
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                                                                                               PRELIMINARY
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                                                                                                   PPT:
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alignment_scores:
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                                                                                                                        seq_documentation_block:
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Percent Similarity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 usi_{09-832-658-7} \times 065341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          correlates to differences in sucress accumulation in sugarcame.")
Submitted (MAY 1998) to the EMRL/2008OnF/1008 49+Abases.
-i- CATALYTIC ACTIVITY: BYDWOLVSIS OF TERRIDAL BON-PERMOING BETA-D-FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharum robustum.
Eukaryota; Viridiplantae: Streptophyta: Embryophyta; Tracheophyta:
Spermatophyta; Magnoliophyta: Liliopsida: Poales; Poaceae; PACC clade:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001362; Glycc_hydro_32; pram; pr00251; Glycc_hydro_32; 1; pros; pr00251; pr005051_Er32; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Differential expression of soluble acid invertase (SAI) genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Albert H.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID~62334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 567 AA; 62631 MW, 92FF2D018772FBB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. MOLOKAL 5829; TISSUE-STEM APEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Panicoideae; Andropodoneae, Saccharum
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NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES: EMBL; AF062734; AAC16654.1: -
                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TYEMBLIEL 07, Created)
01-AUG-1998 (TYEMBLIEL 07, Last sequence update)
01-DEC-2001 (TYEMBLIEL 19, Last annotation update)
SOLUBLE ACTU INVERTASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 GlyMetAspAspAspArgHisAspTyrCysAlaLeuClyArgTyrAspAl 274
                                                                                                                                                                                                                                                                                                                                          Saccharum officinarum (Sugarcane).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magmoliophyta: Liliopsida: Foales: Pouceae: PACC clade:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 aAlaAlaAsn 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       065342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            065342
                                                                                                                                        -:- SIMILARITY: HELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES EMBL; AF062735; AAC16655.1: \cdot\cdot
                                                                                                                                                                                                              "Differential expression of soluble acid invertase (SAI) denos
                                                                                                                                                                                                                               STRAIN=CV. LOUISIANA PURPLE: TISSUE=STEM APEX: Albert H.H., Zhu Y.J., Moore P.H.:
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       NCBI_Tax1D=4547;
                                                                                                                                                                                                                                                                                                                         Panicoideae; Andropogoneae; Saccharum
 SEQUENCE
                   Plam, Pt00251; Glyco_Eydro_32; 1.
PROSTTE; PS00609; GLYCOSYL_HYDROT_E$2; 1.
Glycopictein; Glycosidase; Hydrolase.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 TTCTAGCAAT 62
                                                                                         InterPro:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GGAGACGATGATGACAAGATGGCTTACGCCCGCTCTTCGAGGCCCTACAAG<sup>1 G</sup>2
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                                                                                         IPR001362; Glyco_hydro_32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , zhu Y.J., Moore P.H.
567 AA; 62637 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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     47A1FC84CFEB2AFB CRC64;
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MAY 2.5 (FEMMATER: 18, Steated)
*! MAY 2500 (FEMMATER: 18, Steated)
! HIN 2504 (FEMMATER: 17, Last annotation update)
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Eachs W., Methenheiter 1.0.,
"DAA sequence of the BL6 to HL2d genes of intections laryngotracheitis
ricus and characterization of the HL1D gene product as a
maniprospitied and pagessectial virtem protects.":
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                                                                                                                                                                                                                                                                                                                                                                                      111 11 117
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Alphabergesminera (Varion II) sirus.
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RA Dodson K., Domp L.E., Downes M., Dugan-Rocha S., Dunkov B.G., Dunn P., RA Dodson K., Domp L.E., Downes M., Dugan-Rocha S., Dunkov B.G., Dunn P., RA Borrier C., Gabrielian A.E., Garraz C., Perraz C., Perriera S., Eleischmann W., RA Rosler C., Gabrielian A.E., Garraz C., Perraz C., Perriera S., Eleischmann W., RA Rosler C., Gabrielian A.E., Garraz C., Perraz C., Perriera S., Eleischmann W., RA Glodek A., Golyg F., Gorral J.H., Gu Z., Golbart W.M., Glasson K.A., Rorrad J.H., Bu Z., Gunn P., Harris R., Rarris R., Harris R., L., Harvey D., Heiman T.L., Hersandow I.E., Power V., RA Hostin D., Houston K.A., Howland T.J., Rei M.-H., Ibeqwam C., RA Kimmel B.E., Kealnsh F., Karren G.H., Ke Z., Eennisen I.A., Fordow K.A., RA Kimmel B.E., Kealnsh F., Karren G.H., Ke Z., Eennisen I.A., Fordow K.A., RA Kimmel B.E., Kealnsh J., McHeod M.P., McHeod M.P., McHeoton D., RA Kimmel B.E., Kealnsh J., McHeod M.P., McHeoton D., Nelson D.I., RA Morkilov G., Milshina N.V., Mobarry G., Morris J., Moshreti A., RA Morkilov G., Milshina N.V., Mobarry G., Morris J., Moshreti A., RA Morkilov G., Milshina N.V., Mobarry G., Morris J., Moshreti A., RA Morkilov G., Milshina N.V., Mobarry G., Morris J., Moshreti A., RA Morkilov G., Milshina N.V., Mobarry G., Morris J., Moshreti A., Ra Reinert C., Siden Kiames I., Simpsen M., Schert D.F., Duri V., Reese M.G., RA Reinert C., Standets K.D., Scherler F., Sheth I., RA Reinert C., Turner R., Vented E., Mand R., Ville X., Shith H., RA Zhong X.H., Zhong F.N., Zhong W., Zhon S., Zhu S., Zhu X., Shith H.O., Ribos R., Milshina N., Robin G.M., Vented E., Mand Q., Zhed I., RA Zhong X.H., Zhong F.N., Zhong W., Zhong X., Zhu X., Shith H.O., Ribos Remann J., Robin G.M., Vented E., Mand Q., Zhed I., Ra Gibbs R.A., Robin G.M., Vented J., Mand Q., Zhed H., Ra Gibbs R.A., Robin G.M., Vented J., Mand Q., Zhed H., Ra Gibbs R.A., Robin G.M., Vented J., Robin 
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-i- FUNCTION: MAY HE INVOLVED IN CELL ADDESION.
-i- SUBCELLULAR LOCATION: TYPE I MISSISANE PRODER (PERMITAL).
-i- SIMILARTY: BELONGS TO THE CADDERIN FAMILY.
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Brandon R.C., Kogers Y.-H.C., Blaze) R.G., Champe M., Pteitter B.D.
Wan K.H., Doyle G., Baxter E.G., Helt G., Nelson C.R., Mikios G.L.
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Amanatides F.J., Scherer S.E., Li E.W., H. Gias E.A., Talic G.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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Eteryqota: Neoptera: Endopteryqota: Diptera: Brachycera: Museomarpha:
Ephydroidea: Drosophilidae: Drosophila.
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HSSP; P15116; INCJ.
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CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                  prosophila melanodaster (Fruit 11y).
Bikaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
Preryacta: Neophera: Endopheryacta: Diptera: Brachycera: Muscomorpha:
Ephydroidea: Drosophilidae: Drosophila.
NYHLIAXID 7227:
                                                                                                                                                                                                                                                                                                                                                                01-MAK-2001 (TrEMBLrel. 16, Created)
01-MAK-2001 (TrEMBLrel. 16, Last sequence update)
01-DEF-2001 (FrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 CAGGAGGTTCTGACACTGAAAATTGCTAGAAAGTTGTTAGGGGCTCCAAGAG 34
                                                                                                 "A novel member of the Drosophila cadherin superfamily, Cad890 ";
Submitted (JAN 2001) to the ENR./Gauback/20041 darabases
-! SIMILARITY: CONTAINS 12 CADBERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 COOCGIAAGCCATCTTGTCATCATCGTCTCC 3
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                   FlyBase: FBqn0038439; Cad89D.
                                                                             EMBL: AB053260; BAB20634.1:
                                                           HSSP; P15116; INCJ
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[PR000504: RRM.
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CADHERIN 8.
CADHERIN 9.
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PRINTS; PR00205; CADHERIN.
SMART; SM00112; CA; 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 CAGGAGCTTCTGACACTGAAAATTGCTAGAAAACTTGTAGGGGCTCCAAGAG
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NADH DEHYDROGENASE SUBUNIT 2.
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MEDLINE-21085666; PubMed-11217857;
                                                                                                                                                                                                                                                                                                                                                                                                            Apteryx
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                                                                                                                                                                                                                                                                                                               "Complete mitochondrial genome sequences of two extinct mous clarity
                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                      Mitochondrion; NAD; Oxidoreduce
SEOUENCE 346 AA; 38307 MW;
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          7 ACGATGATGACAAGATGGCTT....ACGCCGCTCTTGGAGCCCTACAAGCT 53
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Ratio:
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Both: 2152 Gaps: 1
Bothset Similarity: To. Qui Percent Identity: 41, 45
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EMMOL ALTHOUGES (Abb 1884).

Interpret Phonogloss Collin Abb.

Phonogloss (All Collin Abb. 1).

EMMOL SESSION (Add 1).

EMMOL SESSION (Add 1).

EMMOL SESSION (Add 1).
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Keen B.H., Textiferewakh P.L., Paul D.L., Goodeneauth D.A.;
"Leadaum specialist expression of the neuronal E actin binding protein,
Institution in specialized ordis of stomach and kidney epithelia.";
"Textifer 11:00000 (2003).
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Mammadia: Putheria: Rodentia: Sciuroquathi: Muridae: Murimae: Mus
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of DEC 2001 (FEMBLECL 15, Last sequence aparts)
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Bokuryeti: Metisor; Chordata: Chandata: Vertebrata: Enteleostomi;
Manumalia: Futberia: Erimates: Catarrhini; Hominidae; Homo.
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**I TRI Jose (TEMMSLEEL 17, Last annotation update)

HYP THEIT AL '11.6 KFA PROTEIN.
                                                                                                                                                                                                            WILLIAM COLOUTY TO PARMON TO COME
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o70205;
01-AUG-1998 (TrEMBLEEL 07, Created)
01-AUG-1998 (TrEMBLEEL 07, Last sequence update)
01-DEC-2001 (TrEMBLEEL 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausborg R.;
Strausborg R.;
Sulffiles (AMP 2021) to the TMRE Asenburk/2008 databases
SMBL: BC006714: AAH06714.1; t.
SEQUENCE 660 AA; 72416 MW; 95375D0529940689 CRC64:
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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SMART; SM00102; ADF; 1.
SEQUENCE 660 AA; 72389 MW; PR6F4R9F2A93BH27 CRC54;
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Mammalia: Eutheria: Rodentia: Sciuroquathi: Muridae: Muridae: Mus
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7:302_C/ptodata/2/144/5A_COMB.pep.US-07-801-164A-4 .
7:302_C/ptodata/2/144/5A_COMB.pep.US-07-801-164A-3 .
7:302_C/ptodata/2/144/5A_COMB.pep.US-08 968-747-21 .
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APPLICANT: Calo, Kichard L
APPLICANT: Pepinsky, Blake R
APPLICANT: Chow, Pingchang E
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BYPOTHETICAL: NO
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release
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STREET: Fish & Neave, 125! Avenue of the Americas
CITY: New York
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                                                           71 FOAGAAGSTGCTGTGG 86
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REGISIKALLON NUMBER: 27,
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CLASSIFICATION:
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Patent No. 5084129
                                                       STOREGAL INFORMATION:
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APPELICANT:
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APPERCATION NUMBERS - PRINT DATE: OF JUL 1993
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compatible
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software: Fattem: Fatter
software: Fatter in Release #1.0, Version #1.25
NUFBER APPLICATION TAIA
APPLICATION IN MEMBER 1857-97-0-27,453
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RETEMBATION NUMBER: 66,1
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81.818 Fedcent Identity: 77.273
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FELLING BAFE: 07/980,525
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Percent Similarity: 81.818
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THLEFAX: (510) 655-8542
THLEFAX: (510) 650-8542
INFORMATION FOR SHO ID NO: 1:
SHOULENCE CHARACTERISTICS:
                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                            APPLICANT: Guelz, Susan E
APPLICANT: Cate, Richard L
APPLICANT: Pepinsky, Hlake R
APPLICANT: Chow, Pingchang E
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                                                      STREET: Fish & CITY: New York
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REGISTRATION NUMBER: 3
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                                                                           Fish & Neave, 1251 Avenue of the Americas
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                                                                                                     James F. Haley, Jr
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SOFTWARE, Patentin Release #1.0. Version #1.25 CURRENT APPLICATION DAIA:

115 we will 248

CLASSIFICATION:
PRIOR APPLICATION DATA:
ASPELICATION NUMBER:

08/475.774

FILING DATE: PERSONAL RESTREAMENTS MEDIUM TYPE: Floppy disk

COMPUTER: 18M PC compatible OPERATING SYSIEM: PC-DOS/MS-DOS

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Ratio: 4.944 Gaps: 0
Percent Similarity: 81.818 Fercent Edentity: 77 273
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CHERENI APPLICATION NUMBER: US/17/397,992A CHERENI APPLICATION NUMBER: 1999-09-16 PRIOR APPLICATION NUMBER: 60/101,012 PRIOR APPLICATION NUMBER: 60/118,578 PRIOR FILING DATE: 1999-02-05 PRIOR FILING DATE: 1999-07-08 PRIOR FILING DATE: 1999-07-08 NUMBER: 0F SEQ 10 NOS: 33 NUMBER: FASISED TOR WINDOWS Version 3.0 SOFTWARE: FASISED TOR WINDOWS Version 3.0
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REGISTRATION NUMBER: 27,794
REFERENCY OFFICE MIMBER: BI
TELEYOMMUNICATION INFORMATION:
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MOLECULE IYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: TOPOTHETICAL: NO
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3-912-768-1
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                                                            HYPOTHETICAL:
ANTI-SENSE: NO
FCT US95-93206-1
              alignment_scores:
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                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT: Gool z. Susan E
APPLICANT: Cate, Richard L
APPLICANT: Pepinsky, Blake R
APPLICANT: Chow, Pingchang E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Novel Mateins Of IEN-Heta NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-FOS
SOPTWARE: Patentin Release #1.0. Version #1.25
CHERENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US35/03206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE. Floppy disk
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                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION.
ATTORNEY/AGENT INFORMATION:
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STREET: Fish & Neave, 1251 Agenue of the
STREET: Americas
CITY: New York
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MOLECULE TYPE: Pr
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                                                                                                                                                                                                                                                                                                    NAME: Haley Jr., James REGISTRATION NUMBER: 2
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ETILE OF INVERTOR, BODILAS O.
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                                                                                               APPLICANT: SUCANC, HARSE, BURANATOU, MASAMISTANTOUCHT
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22202
                                                                                                          Virginia.
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1755 S. Jefferson Davis Highway, Suite 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Sequence 3, Application US/08912768 ; Patent No. 6127332
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Ratio: 4.944 Gaps: 0
Percent Similarity: 81.818 Percent identity: 77.278
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TILLIX. 248855 OPAT UR
INFORMATION FOR SEQ 1D NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                          APPLICANT: Goelz, Susan E
APPLICANT: Cate, Richard I.
APPLICANT: Pepinsky, Blake B
APPLICANT: Chow, Pinachana E
APPLICANT: Chow, Pinachana E
APPLICANT: Chow, Pinachana E
APPLICANT: Chow, Pinachana E
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REFERENCE/POCKET NUMBER: 1126 (
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Ploppy of COMPUTER: IBM PC com
CURRENT APPLICATION DATA:
                                                                                                                   COMPUTER READABLE FORM:
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                                     MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                              ADDRESSEE: James F. Haley, Jr.
STREET: Fish & Reave, 1251 Avenue of the Americas
STYY. H. & Y.J.k
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OTHER INFERMATION: ZHOTO "HE-IEN-beta"
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                         SOFTWARE:
                                                                                                                                                                     COUNTRY:
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APPLICATION NUMBER: 05/08/012.768

CLASSIFICATION:

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Percent Similarity: 81.818 Fercent Identity: 77.273
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Alian seq 1/1 to: US-09-206-903A-9 from: 1 to: 187
                                                                                                                                                                                              Ratio: 4.944
Percent Similarity: 81.818
                                                                                     08 \cdot 09 - 832 \cdot 658 \ 7 \times 08 \cdot 09 \cdot 206 \cdot 903A \cdot 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID No 9
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COURGENT APPLICATION NUMBER: 183/03/206,903
COURGENT FILING DATE: 1998-12-07
FRIOR APPLICATION NUMBER: 08-60/186,463
PRIOR FILING DATE: 1998-10-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT: Chen, Jian
APPLICANT: Godowski, Faul J.
APPLICANT: wood, William 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BENERAL INFORMATION:
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TELEFAX: (212) 596-9000
(NPGHMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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US-08-406-030A-30
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                                                                                                                  REFERENCE/DOCKET NUMBER: TK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9940
INFORMATION FOR SEQ ID NO: 30:
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APPLICATION NUMBER: US 07/985,586

FILLING DATE: 03-DEC-1992
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FILING DATE: 05-NOV-1992
ATTORNEY/AGENT INFORMATION:
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- US 09 832 658+7 x US 09 206 936 7
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: SEQ ID NO 7
: LENGTH: 187
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; Sequence 7, Application US/09206946A
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Percent Similarity: 81.818 Percent Identity: 77.278
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EARLIER APPLICATION NUMBER: 60/084,045
EARLIER FILING DATE: 1998-05-04
NUMBER OF SEQ ID NOS: 24
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EARLIER APPLICATION NUMBER: US 60/067,897
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APPLICANT: Wood, William I.
TITLE OF INVENTION: No. 6300475el Intereron
FILE REPERENCE: P1224R1
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TYPE: PRT
ORGANISM: Homo sapiens
                                                  38 sGlnLysLeuLeuTrp 43
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